

REMARKS

Claims 1-6, 10-16, and 20 are in this application. Claims 7 9 and 17-19 have been canceled.

The specification has been amended at paragraphs 0006 to incorporate prior art teaching reflecting the state of the skill of those having skill in the relevant art and at paragraph 0039 to provide clarity as requested by the Examiner and to provide clear antecedent basis.

Claims 1, 2, 4-6 have been amended to remove the words "of data handling".

Claims 1-6, 10 - 16 and 20 have been rejected under 35 U.S.C. 101. This rejection is respectfully traversed on the ground that the claims indeed do describe a method and a program product that produce a concrete, tangible and useful result. As evidenced by the references incorporated by reference in addition to applicants teachings in the background art, users in the medical profession find great value and usefulness that is tangible and concrete in methods for finding similar gene expression profiles. A problem existing in the prior art for finding such similar gene expression profiles is that current methods of discovering functional similarity in genes use only the intensity of expression. However, the intensity of gene expression can vary with time and follows a specific pattern. For example, progression through the eukaryotic cell cycle is known to be both regulated and accompanied by characteristic periodic fluctuations in the expression levels of numerous genes. Thus a better method was needed to find gene expression profiles in a data base of profiles that were indeed similar

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and applicants have invented such a method which they claim in clear concise and unambiguous language that has not been found to be anticipated or made obvious by any cited prior art teaching of which there are significant amounts extant.

It is well known in the art as exemplified throughout the teachings of the references incorporated by reference that users in the medical profession receive output from computer input/output devices such as applicants teach in their preferred embodiment. See for example 6,406,853 abstract and claims 25, 26 and 6,436,642 column 26 beginning at line 15. It is furthermore clear from such prior art that applicants addition of the step of providing such output to satisfy the Examiner's narrow reading of the claims is not new matter but is supported in their specification by teachings allowing anyone skilled at a rudimentary level of using a computer to make and use the invention and understand the scope of the claims.

Claims 1, 2, 4-6 have been rejected under 35 USC 112 2nd paragraph due to indefinite "handling data". The words "handling data" have been removed from these claims.

Regarding claims 1, 2, 4, 6, 12, 14, 16 and 20, the Examiner has questioned the meaning of the word subsequence. The Examiner is respectfully referred to applicants' specification paragraphs 48 - 50 and to applicants' Figures 4 and 6 where subsequences are described with respect to portions of the data shown in these figures. In addition, paragraph 39 has been amended to include the claim language to provide more clarity and antecedent basis. It is believed that this explanation is

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complete and any outside explanation presented here by applicants' attorney may raise an issue of new matter.

Claim 3 has been rejected as having insufficient antecedent basis for the word "the". The offending word "the" has been removed from the claim.

Claims 1 - 6 and 20 are rejected under 35 USC 112 1st paragraph as not being described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the invention was filed, had possession of the claimed invention. This is asserted as a new matter rejection.

Applicants respectfully traverse these assertions. These claims define methods for determining similarity between gene expression profiles, or portions thereof and creating lists of similar genes. As explained with respect to the foregoing 101 rejection, it is well known in the medical art to access databases and find similar gene expression profiles for the useful purposes of drug discovery as well as disease diagnosis. The incorporation by this amendment of pre-existing patents by reference containing supporting evidence of the relative skill in the relevant art, makes clear that the recitation of output of the result of applicants' novel method steps is well known to anyone who has used a computer as applicants employ and describe in their figure 8.

Applicants note that their claims have not been found to be anticipated nor obvious and applicants and their attorney know of no prior art which could be interpreted to anticipate or make their claimed invention obvious.

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Accordingly it is believed that the claims are now clear, statutory and definite and are drawn to a novel and unobvious method and program product for clustering gene expression profiles which result is concrete, tangible and directly useful in drug selection and disease diagnosis. An early issue date will be appreciated.

Respectfully submitted,

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